RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/826812

Source: 1FUO

Date Processed by STIC: 11-30-4

ENTERED

RAW SEQUENCE LISTING   DATE: 11/30/2004
PATENT APPLICATION: **US/10/826,812**   TIME: 15:30:15

Input Set : **N:\Crf3\RULE60\10826812.raw**
Output Set: **N:\CRF4\11302004\J826812.raw**

SEQUENCE LISTING

```
 1 (1)  GENERAL INFORMATION:
 2      (i)  APPLICANT: Goodman, Corey S.
 3                      Kidd, Thomas
 4                      Mitchell, Kevin
 5                      Tear, Guy
 6     (ii)  TITLE OF INVENTION: Robo: A Novel Family of Polypeptide and
 7                               Nucleic Acids
 8    (iii)  NUMBER OF SEQUENCES: 13
 9     (iv)  CORRESPONDENCE ADDRESS:
10           (A)  ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
11           (B)  STREET: 75 DENISE DRIVE
12           (C)  CITY: HILLSBOROUGH
13           (D)  STATE: CALIFORNIA
14           (E)  COUNTRY: USA
15           (F)  ZIP: 94010
16      (v)  COMPUTER READABLE FORM:
17           (A)  MEDIUM TYPE: Floppy disk
18           (B)  COMPUTER: IBM PC compatible
19           (C)  OPERATING SYSTEM: PC-DOS/MS-DOS
20           (D)  SOFTWARE: PatentIn Release #1.0, Version #1.30
21     (vi)  CURRENT APPLICATION DATA:
```
C--> `22           (A)  APPLICATION NUMBER: US/10/826,812`
C--> `23           (B)  FILING DATE: 16-Apr-2004`
W--> `29           (C)  CLASSIFICATION:`
```
26    (vii)  PRIOR APPLICATION DATA:
27           (A)  APPLICATION NUMBER: US/08/971,172
28           (B)  FILING DATE: 14-Nov-1997
31   (viii)  ATTORNEY/AGENT INFORMATION:
32           (A)  NAME: OSMAN, RICHARD A
33           (B)  REGISTRATION NUMBER: 36,627
34           (C)  REFERENCE/DOCKET NUMBER: B98-006
35     (ix)  TELECOMMUNICATION INFORMATION:
36           (A)  TELEPHONE: (650) 343-4341
37           (B)  TELEFAX: (650) 343-4342
38 (2)  INFORMATION FOR SEQ ID NO: 1:
39      (i)  SEQUENCE CHARACTERISTICS:
40           (A)  LENGTH: 4188 base pairs
41           (B)  TYPE: nucleic acid
42           (C)  STRANDEDNESS: double
43           (D)  TOPOLOGY: linear
44     (ii)  MOLECULE TYPE: cDNA
45     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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46   ATGCATCCCA TGCATCCCGA AAACCACGCC ATCGCCCGGA GCACGAGCAC CACTAATAAC     60
47   CCATCTCGCA GTCGGAGCAG CAGGATGTGG CTCCTGCCCG CCTGGCTGCT CCTCGTCCTG    120
48   GTGGCCAGCA ATGGCCTGCC AGCAGTCAGA GGCCAGTACC AATCGCCACG TATCATCGAG    180
49   CATCCCACGG ATCTGGTCGT TAAGAAGAAT GAACCCGCCA CGCTCAACTG CAAAGTGGAG    240
50   GGCAAGCCGG AACCCACCAT TGAGTGGTTT AAGGATGGCG AACCCGTCAG CACCAACGAA    300
51   AAGAAATCGC ACCGCGTCCA GTTCAAGGAC GGCGCCCTCT TCTTTTACAG GACAATGCAA    360
52   GGCAAGAAGG AGCAGGACGG CGGAGAGTAC TGGTGCGTGG CCAAGAACCG AGTGGGCCAG    420
53   GCCGTTAGTC GCCATGCCTC CCTCCAGATA GCTGTTTTGC GCGACGATTT TCGCGTGGAG    480
54   CCCAAAGACA CGCGAGTGGC CAAAGGCGAG ACGGCTCTGC TGGAGTGTGG GCCGCCCAAA    540
55   GGCATTCCAG AGCCAACGCT GATTTGGATA AAGGACGGCG TTCCCTTGGA CGACCTGAAA    600
56   GCCATGTCGT TTGGCGCCAG CTCCCGCGTT CGAATTGTGG ACGGTGGCAA CCTGCTGATC    660
57   AGCAATGTGG AGCCCATTGA TGAGGGCAAC TACAAGTGCA TTGCCCAGAA TCTGGTAGGC    720
58   ACCCGCGAGA GCAGCTATGC CAAGCTGATT GTCCAGGTCA AACCATACTT TATGAAGGAG    780
59   CCCAAGGATC AGGTGATGCT CTACGGCCAG ACAGCCACTT TCCACTGCTC AGTGGGCGGT    840
60   GATCCGCCGC CGAAAGTGTT GTGGAAAAAG GAGGAGGGCA ATATTCCGGT GTCCAGAGCG    900
61   CGAATCCTTC ACGACGAGAA AAGTTTAGAG ATATCCAACA TAACGCCCAC CGATGAGGGC    960
62   ACCTATGTCT GCGAGGCACA CAACAATGTC GGTCAGATCA GCGCTAGGGC TTCTCTTATA   1020
63   GTCCACGCTC CGCCGAACTT TACGAAAAGA CCCAGTAACA AGAAAGTGGG ACTAAATGGG   1080
64   GTTGTCCAAC TACCTTGCAT GGCCTCCGGA AACCCTCCGC CGTCTGTATT CTGGACCAAG   1140
65   GAAGGAGTAT CCACTCTTAT GTTCCCAAAT AGTTCGCACG GAAGGCAGTA TGTGGCTGCC   1200
66   GATGGAACTC TGCAGATTAC GGATGTGCGG CAGGAAGACG AAGGCTACTA TGTGTGTTCC   1260
67   GCTTTCAGTG TAGTCGATTC CTCTACAGTA CGGGTTTTCC TGCAAGTCAG CTCGGTAGAC   1320
68   GAGCGTCCAC CTCCGATTAT TCAAATCGGA CCTGCCAATC AAACACTGCC CAAGGGATCA   1380
69   GTTGCTACTT TACCCTGTCG GGCCACTGGA AATCCCAGTC CCCGTATCAA GTGGTTCCAC   1440
70   GATGGACATG CCGTACAAGC GGGCAATCGA TACAGCATCA TCCAAGGAAG CTCACTGAGA   1500
71   GTCGATGACC TTCAACTAAG TGACTCTGGT ACCTACACCT GCACTGCATC TGGCGAACGA   1560
72   GGAGAAACTT CCTGGGCTGC CACACTAACG GTGGAAAAAC CCGGTTCTAC ATCTCTTCAC   1620
73   CGGGCAGCTG ATCCTAGCAC TTATCCTGCT CCTCCAGGAA CACCTAAAGT CCTGAATGTC   1680
74   AGTCGCACCA GCATTAGTCT TCGTTGGGCT AAAAGCCAAG AGAAACCCGG AGCTGTGGGC   1740
75   CCAATCATTG GATACACTGT AGAGTACTTC AGTCCGGATC TGCAAACTGG TTGGATTGTG   1800
76   GCTGCCCATC GAGTCGGCGA CACTCAAGTC ACTATCTCGG GTCTCACTCC TGGCACTTCG   1860
77   TATGTGTTCC TAGTTAGAGC TGAGAATACT CAGGGTATTT CTGTGCCTTC CGGCTTATCA   1920
78   AATGTTATTA AAACCATTGA GGCAGATTTC GATGCAGCTT CTGCCAATGA TTTGTCAGCA   1980
79   GCTCGAACTT TGCTGACAGG AAAGTCGGTG GAGCTAATAG ATGCCTCGGC TATCAATGCT   2040
80   AGTGCCGTTA GACTTGAGTG GATGCTCCAC GTGAGCGCTG ATGAGAAATA CGTAGAGGGC   2100
81   CTGCGCATAC ACTATAAGGA TGCCAGTGTA CCATCCGCAC AGTATCACTC GATCACTGTT   2160
82   ATGGATGCCT CTGCAGAATC GTTTGTGGTG GGAAACCTTA AGAAGTACAC CAAGTATGAG   2220
83   TTCTTCCTAA CACCCTTTTT TGAGACAATT GAAGGACAGC CCAGTAACTC CAAGACAGCC   2280
84   CTCACCTATG AAGATGTTCC CTCCGCACCA CCGGATAACA TTCAGATTGG CATGTACAAC   2340
85   CAAACAGCCG GTTGGGTGCG TTGGACTCCG CCACCCTCCC AGCACCACAA TGGCAATTTG   2400
86   TATGGCTACA AGATTGAGGT CAGCGCCGGT AACACCATGA AGGTGCTGGC CAATATGACT   2460
87   CTTAATGCTA CCACCACATC TGTGCTCCTA AATAACCTAA CCACCGGAGC TGTGTACAGC   2520
88   GTGAGGTTGA ACTCCTTTAC CAAGGCAGGA GATGGACCTT ACTCCAAACC GATATCACTA   2580
89   TTCATGGACC CCACCCATCA TGTGCATCCG CCACGGGCAC ATCCAAGCGG CACCCATGAT   2640
90   GGGCGACATG AGGGACAGGA TCTCACGTAT CATAACAATG GCAACATACC ACCTGGCGAC   2700
91   ATTAATCCCA CCACTCATAA AAAGACCACT GACTACCTAT CTGGACCGTG GCTAATGGTG   2760
92   CTGGTCTGCA TCGTTCTTCT AGTCCTGGTT ATTTCGGCGG CTATTTCGAT GGTCTACTTC   2820
93   AAGCGCAAGC ATCAAATGAC CAAGGAATTG GGTCACTTAA GTGTGGTCAG TGACAACGAA   2880
94   ATAACCGCAT TAAATATCAA TAGCAAAGAG AGCCTTTGGA TAGACCATCA TCGTGGATGG   2940
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 95     CGAACTGCCG ATACTGACAA AGACTCAGGA TTAAGCGAAT CGAAGCTACT ATCCCACGTT    3000
 96     AACAGCAGTC AATCCAACTA CAATAACTCC GATGGAGGAA CCGATTATGC AGAAGTTGAC    3060
 97     ACCCGTAACC TTACCACCTT CTACAATTGT CGCAAGAGCC CCGATAATCC CACGCCGTAC    3120
 98     GCCACCACTA TGATCATTGG TACCTCTTCC AGTGAGACCT GCACCAAGAC AACATCTATA    3180
 99     AGTGCCGATA AGGACTCGGG AACTCATTCG CCCTATTCTG ACGCATTTGC CGGTCAGGTG    3240
100     CCAGCGGTTC CTGTTGTCAA ATCCAACTAT CTTCAGTATC CGGTTGAACC GATCAACTGG    3300
101     TCAGAGTTTC TACCCCCGCC GCCAGAACAC CCACCTCCGT CTTCTACCTA TGGATACGCA    3360
102     CAAGGATCTC CTGAATCTTC GCGGAAGAGC TCCAAAAGCG CAGGTTCCGG CATTTCTACA    3420
103     AATCAAAGCA TTCTGAACGC ATCCATACAC AGCAGCTCCT CGGGCGGCTT TTCAGCTTGG    3480
104     GGAGTATCGC CCCAATATGC TGTCGCCTGT CCACCGGAAA ACGTTTATAG CAATCCGCTG    3540
105     TCGGCAGTGG CTGGCGGCAC CCAGAACCGC TATCAGATAA CGCCCACAAA CCAACATCCG    3600
106     CCACAGTTAC CGGCCTACTT TGCCACCACG GGTCCAGGAG GAGCTGTACC ACCCAACCAC    3660
107     CTGCCATTTG CCACACAGCG TCATGCAGCC AGCGAGTACC AGGCTGGACT GAATGCAGCG    3720
108     CGATGTGCCC AAAGCCGCGC CTGCAACAGC TGCGATGCCT TGGCCACACC CTCGCCCATG    3780
109     CAACCCCCAC CGCCAGTTCC CGTACCCGAG GGCTGGTACC AACCGGTGCA TCCCAATAGC    3840
110     CACCCGATGC ACCCGACCTC CTCCAACCAC CAGATCTACC AGTGCTCCTC CGAGTGCTCG    3900
111     GATCACTCGA GGAGCTCGCA GAGTCACAAG CGGCAGCTGC AGCTCGAGGA GCACGGCAGC    3960
112     AGTGCCAAAC AACGCGGAGG ACACCACCGT CGACGAGCCC CGGTGGTGCA GCCGTGCATG    4020
113     GAGAGCGAGA ACGAGAACAT GCTGGCGGAG TACGAGCAGC GCCAGTACAC CAGCGATTGC    4080
114     TGCAATAGCT CCCGCGAGGG CGACACCTGC TCCTGCAGCG AGGGATCCTG TCTTTACGCC    4140
115     GAGGCGGGCG AGCCGGCGCC TCGTCAAATG ACTGCTAAGA ACACCTAA               4188
117  (2) INFORMATION FOR SEQ ID NO: 2:
118      (i) SEQUENCE CHARACTERISTICS:
119          (A) LENGTH: 1395 amino acids
120          (B) TYPE: amino acid
121          (C) STRANDEDNESS: single
122          (D) TOPOLOGY: linear
123     (ii) MOLECULE TYPE: peptide
124     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
125          Met His Pro Met His Pro Glu Asn His Ala Ile Ala Arg Ser Thr Ser
126          1               5                   10                  15
127          Thr Thr Asn Asn Pro Ser Arg Ser Arg Ser Ser Arg Met Trp Leu Leu
128                       20                  25                  30
129          Pro Ala Trp Leu Leu Leu Val Leu Val Ala Ser Asn Gly Leu Pro Ala
130                       35                  40                  45
131          Val Arg Gly Gln Tyr Gln Ser Pro Arg Ile Ile Glu His Pro Thr Asp
132               50                  55                  60
133          Leu Val Val Lys Lys Asn Glu Pro Ala Thr Leu Asn Cys Lys Val Glu
134          65                  70                  75                  80
135          Gly Lys Pro Glu Pro Thr Ile Glu Trp Phe Lys Asp Gly Glu Pro Val
136                       85                  90                  95
137          Ser Thr Asn Glu Lys Lys Ser His Arg Val Gln Phe Lys Asp Gly Ala
138                       100                 105                 110
139          Leu Phe Phe Tyr Arg Thr Met Gln Gly Lys Lys Glu Gln Asp Gly Gly
140                       115                 120                 125
141          Glu Tyr Trp Cys Val Ala Lys Asn Arg Val Gly Gln Ala Val Ser Arg
142               130                 135                 140
143          His Ala Ser Leu Gln Ile Ala Val Leu Arg Asp Asp Phe Arg Val Glu
144          145                 150                 155                 160
```

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145        Pro Lys Asp Thr Arg Val Ala Lys Gly Glu Thr Ala Leu Leu Glu Cys
146                        165             170             175
147        Gly Pro Pro Lys Gly Ile Pro Glu Pro Thr Leu Ile Trp Ile Lys Asp
148                        180             185             190
149        Gly Val Pro Leu Asp Asp Leu Lys Ala Met Ser Phe Gly Ala Ser Ser
150                        195             200             205
151        Arg Val Arg Ile Val Asp Gly Gly Asn Leu Leu Ile Ser Asn Val Glu
152                    210             215             220
153        Pro Ile Asp Glu Gly Asn Tyr Lys Cys Ile Ala Gln Asn Leu Val Gly
154        225             230             235                 240
155        Thr Arg Glu Ser Ser Tyr Ala Lys Leu Ile Val Gln Val Lys Pro Tyr
156                        245             250                 255
157        Phe Met Lys Glu Pro Lys Asp Gln Val Met Leu Tyr Gly Gln Thr Ala
158                        260             265             270
159        Thr Phe His Cys Ser Val Gly Gly Asp Pro Pro Pro Lys Val Leu Trp
160                    275             280             285
161        Lys Lys Glu Glu Gly Asn Ile Pro Val Ser Arg Ala Arg Ile Leu His
162                    290             295             300
163        Asp Glu Lys Ser Leu Glu Ile Ser Asn Ile Thr Pro Thr Asp Glu Gly
164        305             310             315                 320
165        Thr Tyr Val Cys Glu Ala His Asn Asn Val Gly Gln Ile Ser Ala Arg
166                        325             330                 335
167        Ala Ser Leu Ile Val His Ala Pro Pro Asn Phe Thr Lys Arg Pro Ser
168                        340             345             350
169        Asn Lys Lys Val Gly Leu Asn Gly Val Val Gln Leu Pro Cys Met Ala
170                        355             360             365
171        Ser Gly Asn Pro Pro Pro Ser Val Phe Trp Thr Lys Glu Gly Val Ser
172                        370             375             380
173        Thr Leu Met Phe Pro Asn Ser Ser His Gly Arg Gln Tyr Val Ala Ala
174        385                 390             395                 400
175        Asp Gly Thr Leu Gln Ile Thr Asp Val Arg Gln Glu Asp Glu Gly Tyr
176                        405             410                 415
177        Tyr Val Cys Ser Ala Phe Ser Val Val Asp Ser Ser Thr Val Arg Val
178                        420             425             430
179        Phe Leu Gln Val Ser Ser Val Asp Glu Arg Pro Pro Pro Ile Ile Gln
180                    435             440             445
181        Ile Gly Pro Ala Asn Gln Thr Leu Pro Lys Gly Ser Val Ala Thr Leu
182                    450             455             460
183        Pro Cys Arg Ala Thr Gly Asn Pro Ser Pro Arg Ile Lys Trp Phe His
184        465             470             475                 480
185        Asp Gly His Ala Val Gln Ala Gly Asn Arg Tyr Ser Ile Ile Gln Gly
186                        485             490                 495
187        Ser Ser Leu Arg Val Asp Asp Leu Gln Leu Ser Asp Ser Gly Thr Tyr
188                    500             505                 510
189        Thr Cys Thr Ala Ser Gly Glu Arg Gly Glu Thr Ser Trp Ala Ala Thr
190                    515             520                 525
191        Leu Thr Val Glu Lys Pro Gly Ser Thr Ser Leu His Arg Ala Ala Asp
192                    530             535             540
193        Pro Ser Thr Tyr Pro Ala Pro Pro Gly Thr Pro Lys Val Leu Asn Val
```

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194        545                   550                   555                         560
195        Ser Arg Thr Ser Ile Ser Leu Arg Trp Ala Lys Ser Gln Glu Lys Pro
196                        565                   570                   575
197        Gly Ala Val Gly Pro Ile Ile Gly Tyr Thr Val Glu Tyr Phe Ser Pro
198                        580                   585                   590
199        Asp Leu Gln Thr Gly Trp Ile Val Ala Ala His Arg Val Gly Asp Thr
200                        595                   600                   605
201        Gln Val Thr Ile Ser Gly Leu Thr Pro Gly Thr Ser Tyr Val Phe Leu
202              610                   615                   620
203        Val Arg Ala Glu Asn Thr Gln Gly Ile Ser Val Pro Ser Gly Leu Ser
204        625                   630                   635                         640
205        Asn Val Ile Lys Thr Ile Glu Ala Asp Phe Asp Ala Ala Ser Ala Asn
206                        645                   650                   655
207        Asp Leu Ser Ala Ala Arg Thr Leu Leu Thr Gly Lys Ser Val Glu Leu
208                        660                   665                   670
209        Ile Asp Ala Ser Ala Ile Asn Ala Ser Ala Val Arg Leu Glu Trp Met
210                        675                   680                   685
211        Leu His Val Ser Ala Asp Glu Lys Tyr Val Glu Gly Leu Arg Ile His
212              690                   695                   700
213        Tyr Lys Asp Ala Ser Val Pro Ser Ala Gln Tyr His Ser Ile Thr Val
214        705                   710                   715                         720
215        Met Asp Ala Ser Ala Glu Ser Phe Val Val Gly Asn Leu Lys Lys Tyr
216                        725                   730                   735
217        Thr Lys Tyr Glu Phe Phe Leu Thr Pro Phe Phe Glu Thr Ile Glu Gly
218              740                   745                   750
219        Gln Pro Ser Asn Ser Lys Thr Ala Leu Thr Tyr Glu Asp Val Pro Ser
220              755                   760                   765
221        Ala Pro Pro Asp Asn Ile Gln Ile Gly Met Tyr Asn Gln Thr Ala Gly
222              770                   775                   780
223        Trp Val Arg Trp Thr Pro Pro Ser Gln His His Asn Gly Asn Leu
224        785                   790                   795                         800
225        Tyr Gly Tyr Lys Ile Glu Val Ser Ala Gly Asn Thr Met Lys Val Leu
226                        805                   810                   815
227        Ala Asn Met Thr Leu Asn Ala Thr Thr Thr Ser Val Leu Leu Asn Asn
228                        820                   825                   830
229        Leu Thr Thr Gly Ala Val Tyr Ser Val Arg Leu Asn Ser Phe Thr Lys
230                        835                   840                   845
231        Ala Gly Asp Gly Pro Tyr Ser Lys Pro Ile Ser Leu Phe Met Asp Pro
232              850                   855                   860
233        Thr His His Val His Pro Pro Arg Ala His Pro Ser Gly Thr His Asp
234        865                   870                   875                         880
235        Gly Arg His Glu Gly Gln Asp Leu Thr Tyr His Asn Asn Gly Asn Ile
236                        885                   890                   895
237        Pro Pro Gly Asp Ile Asn Pro Thr Thr His Lys Lys Thr Thr Asp Tyr
238              900                   905                   910
239        Leu Ser Gly Pro Trp Leu Met Val Leu Val Cys Ile Val Leu Leu Val
240              915                   920                   925
241        Leu Val Ile Ser Ala Ala Ile Ser Met Val Tyr Phe Lys Arg Lys His
242              930                   935                   940
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 11/30/2004
PATENT APPLICATION: US/10/826,812   TIME: 15:30:16

Input Set : **N:\Crf3\RULE60\10826812.raw**
Output Set: **N:\CRF4\11302004\J826812.raw**

<u>Please Note:</u>
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.**

Seq#:9; N Pos. 855,1186
Seq#:10; Xaa Pos.285,396

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/826,812**

DATE: 11/30/2004
TIME: 15:30:16

Input Set : **N:\Crf3\RULE60\10826812.raw**
Output Set: **N:\CRF4\11302004\J826812.raw**

L:22 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:23 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:29 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:1200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:272
M:341 Repeated in SeqNo=10